GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 16:22:02 ; Search time 210.96 Seconds
(without alignments)
2539.236 Million cell updates/sec

Title: US-09-880-887-9
Perfect score: 312
Sequence: 1 gtttgtttatgcatccttttt.....cgtattcttttacatttcag 312

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
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19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	312	100.0	312	21	AAA99045	Human Factor IX tr
	2	312	100.0	312	22	AAC67922	Human Factor IX tr
	3	146.2	46.9	38059	22	AAF54018	Human factor IX (h
	4	145.4	46.6	1438	24	AAI71003	Human Factor IX ge
	5	115	36.9	10329	24	ABL34122	Human immune syste
c	6	103.6	33.2	10329	24	ABL34123	Human immune syste
	7	92.8	29.7	492	21	AAC71352	Single nucleotide
	8	51.8	16.6	9927	24	ABL32112	Human immune syste
	9	47.6	15.3	162450	21	AAZ86967	Retinoblastoma bin
c	10	39	12.5	2503	15	AAQ53480	pNPX30 xylanase cD
	11	38.6	12.4	6104	24	ABL33367	Human immune syste
	12	37.8	12.1	6350	24	AAS61110	Human gene regulat
	13	37.6	12.1	544	22	AAH33046	Human colon cancer
	14	37.4	12.0	6799	22	AAI58419	Human polynucleoti
	15	37.4	12.0	513445	22	AAI61373	Soybean 318013 reg
c	16	37.2	11.9	6151	24	ABL33610	Human immune syste
c	17	37	11.9	1874	20	AAX61590	B. burgdorferi ant
c	18	37	11.9	2007	20	AAX61589	B. burgdorferi ant
	19	37	11.9	2693	23	ABL24214	Drosophila melanog
	20	37	11.9	6392	24	ABL32684	Human immune syste
	21	37	11.9	6392	24	ABL34506	Human metastasis a
c	22	37	11.9	80331	22	AAC89559	Human histone deac
c	23	37	11.9	111309	20	AAX20250	Borrelia burgdorfe
	24	36.8	11.8	2335	21	AAA97795	Rat stress associa
	25	36.8	11.8	7544	22	AAS45301	Chemically pretrea
	26	36.8	11.8	11790	24	ABL32543	Human immune syste
	27	36.6	11.7	2169	22	AAH15909	Human cDNA sequenc
	28	36.6	11.7	6078	24	ABL33244	Human immune syste
	29	36.6	11.7	8662	24	ABL34637	Human metastasis a
c	30	36.4	11.7	5445	22	AAS46595	Tumour suppressor
	31	36.4	11.7	10957	24	ABL33110	Human immune syste
	32	36.4	11.7	19380	24	AAS61427	Human gene regulat
c	33	36.2	11.6	30803	22	AAK68410	Human immune/haema
	34	36	11.5	6112	24	ABL32488	Human immune syste
	35	36	11.5	16217	24	ABL32625	Human immune syste
	36	35.8	11.5	6112	24	ABL32473	Human immune syste
	37	35.8	11.5	6224	24	ABL33308	Human immune syste
	38	35.8	11.5	12405	22	AAS45330	Chemically pretrea
	39	35.8	11.5	12405	24	AAS61143	Human gene regulat
	40	35.8	11.5	90104	23	ABL12402	Drosophila melanog
	41	35.6	11.4	828	22	AAH05502	Human cDNA clone (
	42	35.6	11.4	5511	24	ABL34001	Human immune syste
	43	35.6	11.4	7128	24	ABL33559	Human immune syste
	44	35.6	11.4	17294	24	ABL32987	Human immune syste
	45	35.4	11.3	425	22	AAS60450	Human cancer agent

ALIGNMENTS

RESULT 1
AAA99045
ID AAA99045 standard; DNA; 312 BP.
XX
AC AAA99045;
XX
DT 17-JAN-2001 (first entry)
XX
DE Human Factor IX truncated intron 1 (FIX TI1) SEQ ID NO:9.
XX
KW Human; Factor VIII; FVIII; Factor IX truncated intron 1; FIX TI1;
KW B-domain; modification; gene therapy; PCR; haemostatic;
KW haemophilia A; ss.
XX
OS Homo sapiens.
XX
PN EP1038959-A1.
XX
PD 27-SEP-2000.
XX
PF 17-MAR-1999; 99EP-0104050.
XX
PR 17-MAR-1999; 99EP-0104050.
XX
PA (AVET) AVENTIS BEHRING GMBH.
XX
PI Negrier C, Plantier JL;
XX
DR WPI; 2000-603721/58.
XX
PT Novel modified factor VIII cDNA for use in gene therapy, in which the
PT wild-type factor VIII cDNA B-domain is deleted and truncated factor IX

PT intron 1 is inserted in one or more locations -
XX
PS Disclosure; Page 9-10; 17pp; English.
XX
CC The present invention describes a modified Factor VIII (FVIII) cDNA (I)
CC characterised in that the B-domain of wild-type FVIII cDNA has
CC been deleted and a truncated Factor IX intron 1 (FIX TI1) has been
CC inserted in one or more locations of FVIII cDNA. Also described
CC are: (1) producing FVIII in a cell line containing (I); and
CC (2) a transfer vector for use in gene therapy comprising (I). (I) has
CC haemostatic activity, and can be used in gene therapy. (I) is used in
CC a transfer vector for gene therapy and for a higher yield in vitro
CC production of FVIII, which is used for treating haemophilia A.
CC Production of FVIII is improved by adding introns in the FVIII. The
CC present sequence represents a the human FIX TI1 sequence which
CC is used in the exemplification of the present invention.
XX
SQ Sequence 312 BP; 96 A; 47 C; 53 G; 116 T; 0 other;

Query Match 100.0%; Score 312; DB 21; Length 312;
Best Local Similarity 100.0%; Pred. No. 6.6e-67;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtttgtttatgcatccttttttaaaatacattgagtatgcttgccttttagatatagaaa 60
Db 1 gtttgtttatgcatccttttttaaaatacattgagtatgcttgccttttagatatagaaa 60

Qy 61 tatctgatgctgtcttcttcactaaattttgattacatgatttgacagcaatattgaaga 120
Db 61 tatctgatgctgtcttcttcactaaattttgattacatgatttgacagcaatattgaaga 120

Qy 121 gtctaacagccagcacgcaggttggtaagtactgtgggaacatcacagattttggctcca 180
Db 121 gtctaacagccagcacgcaggttggtaagtactgtgggaacatcacagattttggctcca 180

Qy 181 tgccctaaagagaaattggctttcagattatttggattaaaaacaaagactttcttaaga 240
Db 181 tgccctaaagagaaattggctttcagattatttggattaaaaacaaagactttcttaaga 240

Qy 241 gatgtaaaattttcatgatgttttcttttttgctaaaactaaagaattaacgcgtattct 300
Db 241 gatgtaaaattttcatgatgttttcttttttgctaaaactaaagaattaacgcgtattct 300

Qy 301 tttacatttcag 312
Db 301 tttacatttcag 312

RESULT 2
AAC67922
ID AAC67922 standard; cDNA; 312 BP.
XX
AC AAC67922;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human Factor IX truncated intron 1.
XX
KW Human; FVIII; Factor VIII; gene therapy; Factor IX intron 1;
KW Factor VIII production; ss.
XX
OS Homo sapiens.
XX
PN EP1048726-A2.
XX
PD 02-NOV-2000.
XX
PF 03-MAR-2000; 2000EP-0104677.
XX
PR 29-APR-1999; 99EP-0107397.
XX
PA (CENT-) CENTEON PHARMA GMBH.
XX
PI Negrier C, Plantier JL;
XX
DR WPI; 2001-072945/09.
XX
PT Modified Factor VIII cDNA comprising a truncated Factor IX intron 1
PT sequence inserted at one or more locations, useful for efficient
PT production of Factor VIII in host cells -
XX
PS Disclosure; Page 11; 19pp; English.
XX
CC The present sequence is used in an invention relating to a modified
CC Factor VIII cDNA having a truncated Factor IX intron 1 inserted at one or
CC more places. The cDNA encodes a mutated Factor VIII, where the wild type
CC B domain has been deleted. The modified Factor VIII cDNA is used to
CC generate Factor VIII protein in vitro. The cDNA is used in a transfer
CC vector for gene therapy. The modification allows increased production of
CC Factor VIII. Truncated Factor VIII cDNA with an insertion of the Factor
CC IX intron 1 in intron 1 and 12 and in intron 1 and 13 gave 2-3 and 8-9
CC times more Factor VIII than unmodified Factor VIII cDNA.
XX
SQ Sequence 312 BP; 96 A; 47 C; 53 G; 116 T; 0 other;

Query Match 100.0%; Score 312; DB 22; Length 312;
Best Local Similarity 100.0%; Pred. No. 6.6e-67;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtttgtttatgcatccttttttaaaatacattgagtatgcttgccttttagatatagaaa 60
Db 1 gtttgtttatgcatccttttttaaaatacattgagtatgcttgccttttagatatagaaa 60

Qy 61 tatctgatgctgtcttcttcactaaattttgattacatgatttgacagcaatattgaaga 120
Db 61 tatctgatgctgtcttcttcactaaattttgattacatgatttgacagcaatattgaaga 120

Qy 121 gtctaacagccagcacgcaggttggtaagtactgtgggaacatcacagattttggctcca 180
Db 121 gtctaacagccagcacgcaggttggtaagtactgtgggaacatcacagattttggctcca 180

Qy 181 tgccctaaagagaaattggctttcagattatttggattaaaaacaaagactttcttaaga 240
Db 181 tgccctaaagagaaattggctttcagattatttggattaaaaacaaagactttcttaaga 240

Qy 241 gatgtaaaattttcatgatgttttcttttttgctaaaactaaagaattaacgcgtattct 300
Db 241 gatgtaaaattttcatgatgttttcttttttgctaaaactaaagaattaacgcgtattct 300

Qy 301 tttacatttcag 312
Db 301 tttacatttcag 312

RESULT 3
AAF54018
ID AAF54018 standard; DNA; 38059 BP.
XX
AC AAF54018;
XX
DT 30-MAR-2001 (first entry)
XX
DE Human factor IX (hFIX) gene, SEQ ID NO:4.
XX
KW Age-related gene regulation; liver-specific; gene expression;
KW human factor IX; hFIX; AE5'; AE3'; age-regulatable expression construct;
KW antisense therapy; gene therapy; thrombosis; cardiovascular disease;
KW diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;
KW osteoarthritis; dementia; ds.
XX
OS Homo sapiens.
XX
PN WO200075279-A2.
XX

PD 14-DEC-2000.
XX
PF 06-JUN-2000; 2000WO-US15728.
XX
PR 09-JUN-1999; 99US-0328925.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Kurachi K, Kurachi S;
XX
DR WPI; 2001-061708/07.
DR P-PSDB; AAB60281, AAB60282, AAB60283, AAB60284, AAB60285, AAB60286,
DR AAB60287, AAB60288, AAB60289.
XX
PT New regulatory elements that control age-related gene expression,
PT useful in gene therapy and for reducing Factor IX expression -
XX
PS Disclosure; Fig 8A-E; 225pp; English.
XX
CC The invention relates to nucleic acid sequences which regulate gene
CC expression in an age-related manner and/or in a liver-specific manner.
CC The invention identifies regions of the human factor IX (hFIX) gene, and
CC a region of the human protein C (hPC) gene, which are age-related
CC regulatory sequences. The hFIX age-related regulatory sequences are
CC designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'
CC UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position
CC 34383-35655 of AAF54018) respectively. These elements act synergistically
CC to increase hFIX levels over the lifespan of an individual; however, they
CC can independently exert effects on hFIX mRNA in an age-related manner,
CC with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX
CC mRNA levels, over time. AE5' also directs liver-specific expression. The
CC hPC gene age-related regulatory sequence is found in the 5' UTR
CC (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements
CC 5'-GAGGAAA-3' and 5'-CAGGAAG-3'. The age-related regulatory sequences of
CC the invention, along with their homologues, variants and fragments, may
CC be used in the construction of recombinant expression vectors for the
CC expression of a desired sequence in an age-related fashion in a host
CC cell. Preferred target genes for expression in such age-regulatable
CC expression vectors include those encoding proteins involved in blood
CC coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
CC anti-coagulants protein C and antithrombin III), human
CC alpha-1-antitrypsin, PEA-3 protein and reporter proteins such as
CC luciferase. Preferred promoters for use in such age-regulatable
CC expression vectors include the human factor IX promoter, the T7 promoter,
CC the T3 promoter and the SP6 promoter. The expression vectors of the
CC invention may be used in gene therapy to provide age- related and/or
CC liver-specific expression of target genes. Age-regulatable constructs may
CC be used in the treatment of such age-related conditions such as
CC thrombosis, cardiovascular disease, diabetes, Alzheimer's disease,
CC Parkinson's disease, cancer, osteoporosis, osteoarthritis and dementia.
CC Specifically, they may be used to express factor IX antisense mRNA in the
CC treatment of thrombotic conditions associated with the natural
CC age-related rise in factor IX expression. Transgenic cells or animals
CC that contain vectors of the invention are useful as models of these
CC diseases, in screening for potential therapeutic agents and for studying
CC normal processes such as ageing and gene expression. Fragments and
CC homologues of age-related regulatory sequences, are useful as probes to
CC detect, isolate or identify other such sequences in samples. The present
CC sequence represents the hFIX gene.
XX
SQ Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 other;

Query Match 46.9%; Score 146.2; DB 22; Length 38059;
Best Local Similarity 81.6%; Pred. No. 3.6e-26;
Matches 169; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 103 tgacagcaatattgaagagtctaacagccagcacgcaggttggtaagtactgtgggaaca 162
Db 9088 taaaagtaaaattgaatttaattcctaaatctccatgtgtatacagtactgtgggaaca 9147

Qy 163 tcacagattttggctccatgccctaaagagaaattggctttcagattatttggattaaaa 222
Db 9148 tcacagattttggctccatgccctaaagagaaattggctttcagattatttggattaaaa 9207

Qy 223 acaaagactttcttaagagatgtaaaatttttcatgatgttttctttttttgctaaaactaa 282
Db 9208 acaaagactttcttaagagatgtaaaatttttcatgatgttttctttttttgctaaaactaa 9267

Qy 283 agaattaacgcgtattcttttacattt 309
Db 9268 agaattattcttttacatttcagtttt 9294

RESULT 4
AAI71003
ID AAI71003 standard; DNA; 1438 BP.
XX
AC AAI71003;
XX
DT 18-MAR-2002 (first entry)
XX
DE Human Factor IX gene intron A.
XX
KW Factor IX; intron A; human; expression cassette; liver;
KW blood clotting; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200198482-A2.
XX
PD 27-DEC-2001.
XX
PF 19-JUN-2001; 2001WO-US19634.
XX
PR 20-JUN-2000; 2000US-212902P.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (UNIW) UNIV WASHINGTON.
XX
PI Miao CH, Kay MA;
XX
DR WPI; 2002-114582/15.
XX
PT Nucleic acid construct for expressing nucleic acid molecules, proteins
PT in mammalian liver cells, has operably linked hepatic locus control
PT element, hepatic promoter, coding sequence, polyadenylation signal and
PT intron -
XX
PS Claim 22; Page 50-51; 64pp; English.
XX
CC The present sequence is that of intron A of the human Factor IX
CC gene. The intron was incorporated into expression cassettes of
CC the invention designed for liver-specific expression of Factor IX.
CC The cassettes also included an hepatic locus control element, an
CC hepatic promoter located 3' to the hepatic locus control element,
CC the Factor IX coding sequence, and a 3' polyadenylation signal
CC (see AAI71003-16). The intron can be located 5' or 3' to the
CC coding sequence, or within the coding sequence. A 5' location has
CC the advantage of minimising the chance of the intron interfering
CC with the function of the polyadenylation signal. Also provided
CC are vectors that include an expression cassette of the invention.
CC These may episomal or integrating vectors, including viral vectors.
CC The vectors are used in a claimed method of ameliorating the
CC symptoms of a disease. A therapeutic amount blood clotting
CC Factor IX is produced in mammalian liver cells for a period of at
CC least 100 days, and preferably at least 500 days. In examples of
CC the invention, human Factor IX was expressed in mouse liver cells
CC following injection of retrovirus-based plasmids that carried the
CC expression cassettes into the tail vein or portal vein, and by
CC direct injection of plasmid DNA into the liver.
XX
SQ Sequence 1438 BP; 475 A; 240 C; 245 G; 478 T; 0 other;

Query Match 46.6%; Score 145.4; DB 24; Length 1438;

```
  Best Local Similarity   86.1%;  Pred. No. 3e-26;
  Matches  161;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy    103 tgacagcaatattgaagagtctaacagccagcacgcaggttggtaagtactgtgggaaca 162
          | | || || ||||||   |    |    | | |   |  |    ||||||||||||||
Db   1236 taaaagtaaaattgaattttaattcctaaatctccatgtgtatacagtactgtgggaaca 1295

Qy    163 tcacagattttggctccatgccctaaagagaaattggctttcagattatttggattaaaa 222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1296 tcacagattttggctccatgccctaaagagaaattggctttcagattatttggattaaaa 1355

Qy    223 acaaagactttcttaagagatgtaaaattttcatgatgttttcttttttgctaaaactaa 282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1356 acaaagactttcttaagagatgtaaaattttcatgatgttttcttttttgctaaaactaa 1415

Qy    283 agaatta 289
          |||||||
Db   1416 agaatta 1422


RESULT   5
ABL34122
ID   ABL34122 standard; DNA; 10329 BP.
XX
AC   ABL34122;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 2095.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07537.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful
PT   for diagnosis and treatment of diseases associated with abnormal
PT   cytosine methylation  -
XX
PS   Claim 1; SEQ ID NO 2095; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention.
XX
SQ   Sequence 10329 BP; 3676 A; 56 C; 2107 G; 4490 T; 0 other;

  Query Match           36.9%;  Score 115;  DB 24;  Length 10329;
  Best Local Similarity   70.3%;  Pred. No. 1.1e-18;
  Matches  154;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy     86 attttgattacatgatttgacagcaatattgaagagtctaacagccagcacgcaggttgg 145
          |||   |||   |   || | || || ||||||  |        |       |  |
Db  10109 attggaatttttttgattaaaagtaaaattgaattttaatttttaaatttttatgtgtat 10168

Qy    146 taagtactgtgggaacatcacagattttggctccatgccctaaagagaaattggctttca 205
            |||| |||||||| || | ||||||||| |  |||   |||||||||||||| ||| |
Db  10169 atagtattgtgggaatattatagattttggttttatgttttaaagagaaattggttttta 10228

Qy    206 gattatttggattaaaaacaaagactttcttaagagatgtaaaattttcatgatgttttc 265
          |||||||||||||||||| ||||| ||| ||||||||||||||||||| ||||||||||
Db  10229 gattatttggattaaaaataaagatttttttaagagatgtaaaattttttatgatgttttt 10288

Qy    266 ttttttgctaaaactaaagaattaacgcgtattctttta 304
          ||||||| ||||| ||||||||||     |  | |||||
Db  10289 ttttttgttaaaattaaagaattatttttttatatttta 10327


RESULT   6
ABL34123/c
ID   ABL34123 standard; DNA; 10329 BP.
XX
AC   ABL34123;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 2096.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07537.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful
PT   for diagnosis and treatment of diseases associated with abnormal
PT   cytosine methylation  -
XX
PS   Claim 1; SEQ ID NO 2096; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention.
XX
```

```
SQ   Sequence 10329 BP; 2681 A; 56 C; 1865 G; 5727 T; 0 other;

  Query Match           33.2%;  Score 103.6;  DB 24;  Length 10329;
  Best Local Similarity  70.2%;  Pred. No. 6.5e-16;
  Matches  139;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy     92 attacatgatttgacagcaatattgaagagtctaacagccagcacgcaggttggtaagta 151
          |||   | |  | | |  || ||| ||   |    |    | | |      |    | ||
Db    215 ATTCTCTTAACTAAAAATAAAATTAAATTTTAATTCCTAAATCTCCATATATATACAATA 156

Qy    152 ctgtgggaacatcacagattttggctccatgccctaaagagaaattggctttcagattat 211
          || |   |||||||| |||||  |||||| ||||||| | |||||  |||||| |||||
Db    155 CTATAAAAACATCACAAATTTTAACTCCATACCCTAAAAAAAAATTAACTTTCAAATTAT 96

Qy    212 ttggattaaaaacaaagactttcttaagagatgtaaaattttcatgatgttttcttttt 271
          ||  |||||||||||| |||||||||| | || |||||||||||| || ||||||||||
Db     95 TTAAATTAAAAACAAAAACTTTCTTAAAAAATATAAAATTTTCATAATATTTTCTTTTTT 36

Qy    272 gctaaaactaaagaatta 289
          |||||||||||| |||||
Db     35 ACTAAAACTAAAAAATTA 18


RESULT   7
AAC71352
ID   AAC71352 standard; DNA; 492 BP.
XX
AC   AAC71352;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism containing sequence #394.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; ds.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US08440.
XX
PR   31-MAR-1999;   99US-0127248.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single
PT   nucleotide polymorphisms, allele-specific oligonucleotides to the genes
PT   are useful for phenotypic correlations, forensics, paternity testing,
PT   medicine and genetic analysis -
XX
PS   Claim 1; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases.
CC   Note: The degenerate codon within the sequence represents the position
CC   of an SNP, for example the letter S represents a polymorphism where the
CC   nucleotide may be C or G.
XX
SQ   Sequence 492 BP; 180 A; 61 C; 83 G; 167 T; 1 other;

  Query Match           29.7%;  Score 92.8;  DB 21;  Length 492;
  Best Local Similarity  89.3%;  Pred. No. 1.6e-13;
  Matches  100;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy    198 ggctttcagattatttggattaaaaacaaagactttcttaagagatgtaaaattttcatg 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ggctttcagattatttggattaaaaacaaagactttcttaagagatgtaaaattttcatg 60

Qy    258 atgttttcttttttgctaaaactaaagaattaacgcgtattcttttacattt 309
          |||||||||||||||||||||||||||||     |    ||| |  |||
Db     61 atgttttcttttttgctaaaactaaagaattattcttttacatttcagtttt 112


RESULT   8
ABL32112
ID   ABL32112 standard; DNA; 9927 BP.
XX
AC   ABL32112;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 85.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07537.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful
PT   for diagnosis and treatment of diseases associated with abnormal
PT   cytosine methylation  -
XX
PS   Claim 1; SEQ ID NO 85; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention.
XX
SQ   Sequence 9927 BP; 3017 A; 50 C; 1946 G; 4914 T; 0 other;
```

```
  Query Match            16.6%;  Score 51.8;  DB 24;  Length 9927;
  Best Local Similarity  49.4%;  Pred. No. 0.0026;
  Matches  134;  Conservative    0;  Mismatches  137;  Indels    0;  Gaps    0;

Qy       2 tttgtttatgcatccttttttaaaatacattgagtatgcttgccttttagatatagaaat 61
           |||  || |  ||  ||||||  | |   |||   |||  | |   ||||  |||| |  |
Db    5467 tttaatttttaatttttttttataataattatttatttagtgatttatttatatattt 5526

Qy      62 atctgatgctgtcttcttcactaaattttgattacatgatttgacagcaatattgaagag 121
           ||    |  |||  | ||   ||  ||||  ||| ||   |||  | | |||||||||
Db    5527 attgttttatgttatttttttatatttttttttttatatttattggtatcgatattgaagtt 5586

Qy     122 tctaacagccagcacgcaggttggtaagtactgtgggaacatcacagattttggctccat 181
           | |       || |   |  ||    |||| | ||            ||||    |  |
Db    5587 tttttgttatagaaataaatttttggagtattttgtttttcgttttttatttattgtttaa 5646

Qy     182 gccctaaagagaaattggctttcagattatttggattaaaaacaaagactttcttaagag 241
             ||  | ||| || ||  | ||| | | || || |   |     |   |    |
Db    5647 atgaggaaatgtaatagggttggaaattttatagagtatagttattatttgattatgaat 5706

Qy     242 atgtaaaattttcatgatgttttcttttttg 272
           | |||| |||| ||| |   |  |||||
Db    5707 ttttaaatttttttatgtttgatatttttttag 5737


RESULT   9
AAZ86967
ID   AAZ86967 standard; DNA; 162450 BP.
XX
AC   AAZ86967;
XX
DT   16-MAY-2000  (first entry)
XX
DE   Retinoblastoma binding protein-7 genomic DNA sequence.
XX
KW   RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
KW   diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
KW   benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
KW   lymphoma; ds.
XX
OS   Homo sapiens.
XX
PN   WO200000607-A1.
XX
PD   06-JAN-2000.
XX
PF   30-JUN-1999;   99WO-IB01242.
XX
PR   30-JUN-1998;   98US-0091315.
PR   10-DEC-1998;   98US-0111909.
XX
PA   (GEST ) GENSET.
XX
PI   Bougueleret L;
XX
DR   WPI; 2000-117170/10.
XX
PT   Novel nucleic acid and polymorphic markers used for diagnosis of
PT   diseases, especially those involving abnormal cell proliferation and
PT   differentiation -
XX
PS   Claim 1; Page 118-163; 223pp; English.
XX
CC   This sequence represents the retinoblastoma binding protein-7 (RBP-7)
CC   genomic sequence of the invention. The RBP-7 coding sequence and
CC   regulatory sequences are useful for the recombinant production of the
CC   protein and for expressing heterologous nucleic acids. Primers and
CC   probes derived from the RBP-7 nucleotide sequence (e.g. AAZ87035-Z87099)
CC   are useful for DNA amplification and detection methods. RBP-7 biallelic
CC   markers (see AAZ86993-Z87034) are useful for diagnosis of disease
CC   related to alteration in the regulation or in the coding regions of the
CC   RBP-7 gene and for prognosis/diagnosis of an eventual treatment with
CC   therapeutic agents, especially agents acting on pathologies involving
CC   abnormal cell proliferation and/or differentiation, these include
CC   thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,
CC   including breast cancer, sarcomas and other neoplasms, bladder cancer,
CC   colon cancer, lung cancer, prostate cancer, various leukaemias, and
CC   lymphomas. RBP-7 antibodies are useful as diagnostic agents.
XX
SQ   Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other;


  Query Match            15.3%;  Score 47.6;  DB 21;  Length 162450;
  Best Local Similarity  50.9%;  Pred. No. 0.046;
  Matches  113;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy       2 tttgtttatgcatccttttttaaaatacattgagtatgcttgccttttagatatagaaat 61
           |||  ||| | |    ||||||||||||| || | | ||| |||  ||||  | || |  |
Db  124881 tttacttacgaagttatttttaaaatacctttattctgcatgctgtttatttttaaatct 124940

Qy      62 atctgatgctgtcttcttcactaaattttgattacatgatttgacagcaatattgaagag 121
           |          ||| ||   || || || | || ||| |   |        || || |
Db  124941 cttaagactgtgctttttaggtatatattaactatatgctgataatatttctttaaaat 125000

Qy     122 tctaacagccagcacgcaggttggtaagtactgtgggaacatcacagattttggctccat 181
           |         |  |  ||       || |  ||||||  | || |   |||||||    ||
Db  125001 tgggtttaagaagaaccaaaagctgaattgatgtgggcatattaaccattttggtagtat 125060

Qy     182 gccctaaagagaaattggctttcagattatttggattaaaaa 223
             |     ||  |||   ||||   ||| ||   |||| |||
Db  125061 atctggtcgactaatgttcttttccatttttattattacaaa 125102


RESULT  10
AAQ53480/c
ID   AAQ53480 standard; cDNA; 2503 BP.
XX
AC   AAQ53480;
XX
DT   30-JUN-1994  (first entry)
XX
DE   pNPX30 xylanase cDNA.
XX
KW   Xylanase; ruminant animals; fungus; paper; pulp; bagasse;
KW   feedstock; rumen; plant fibre; ss.
XX
OS   Neocallimastix patriciarum.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1935
FT                   /*tag=  a
FT                   /product= Xylanase.
XX
PN   WO9325671-A.
XX
PD   23-DEC-1993.
XX
PF   17-JUN-1993;   93WO-AU00294.
XX
PR   17-JUN-1992;   92AU-0002985.
PR   29-JUN-1992;   92AU-0003238.
PR   01-APR-1993;   93AU-0008100.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Xue GP;
XX
DR   WPI; 1994-007529/01.
DR   P-PSDB; AAR44529.
XX
PT   New recombinant fungal xylanase - used for hydrolysis of xylan in
PT   food and pulp and paper industries and for improving ruminant
PT   feed efficiency
XX
PS   Claim 9; Figure 3; 45pp; English.
XX
```

```
CC   The cloned xylanase coding sequence is derived from an anaerobic
CC   rumen fungus.  The xylanase has high specific activity for the
CC   hydrolysis of xylan.  It can be used for treating pulps in the pulp
CC   and paper industry, for treating bagasse for more efficient disposal
CC   or for the treatment of feedstock to improve nutritional value.
CC   Genetically modified xylanase genes can also be used for the
CC   modification of rumen bacteria to improve plant fibre utilisation by
CC   ruminants.
XX
SQ   Sequence 2503 BP; 893 A; 389 C; 517 G; 704 T; 0 other;


  Query Match            12.5%;  Score 39;  DB 15;  Length 2503;
  Best Local Similarity   59.5%;  Pred. No. 2.6;
  Matches   66;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy    201 tttcagattatttggattaaaaacaaagactttcttaagagatgtaaaatttttcatgatg 260
          |||   ||| ||    | ||  |  |    ||  ||   | || ||||||||||| ||
Db   2372 TTTTTTATTTTTCTACTAAATCAATATTTTTTAATTTTTATATTTAAAATTTTCATAATT 2313

Qy    261 ttttctttttttgctaaaactaaagaattaacgcgtattcttttacatttca 311
          |||| |||||| ||||| | | |   |||     |  | ||| |  |||||
Db   2312 TTTTATTTTTTACTAAATCAACACTTTTATATTTTTATATTTAATTTTTCA 2262


RESULT  11
ABL33367
ID   ABL33367 standard; DNA; 6104 BP.
XX
AC   ABL33367;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 1340.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07537.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful
PT   for diagnosis and treatment of diseases associated with abnormal
PT   cytosine methylation  -
XX
PS   Claim 1; SEQ ID NO 1340; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention.
XX
SQ   Sequence 6104 BP; 1932 A; 72 C; 1371 G; 2729 T; 0 other;


  Query Match            12.4%;  Score 38.6;  DB 24;  Length 6104;
  Best Local Similarity   52.1%;  Pred. No. 3.9;
  Matches   86;  Conservative    0;  Mismatches   79;  Indels    0;  Gaps    0;

Qy    139 aggttggtaagtactgtgggaacatcacagattttggctccatgccctaaagagaaattg 198
          ||  |  ||  ||  | |  ||  | | ||||||||  |  |      |||      |
Db   1867 agtataatatatatagagaaaagtttatagattttgtgtgtagttttgaaaatttttat 1926

Qy    199 gctttcagattatttggattaaaaacaaagactttcttaagagatgtaaaatttttcatga 258
            | | | | ||||| |||||  ||  |  |  || ||     || || | ||||  ||
Db   1927 tttataatagtatttagattatgaaatagaatattatttgtttatttatatttttttgt 1986

Qy    259 tgttttctttttttgctaaaactaaagaattaacgcgtattctttt 303
          | ||||  |||||| | |   | ||   || |     | || ||||
Db   1987 ttttttagtttttgtttatttttaatttttttaatttttttatttt 2031


RESULT  12
AAS61110
ID   AAS61110 standard; DNA; 6350 BP.
XX
AC   AAS61110;
XX
DT   29-JAN-2002  (first entry)
XX
DE   Human gene regulation-associated gene oligonucleotide #65.
XX
KW   Human; Gene regulation-associated gene; severe combined immunodeficiency;
KW   cardiac damage; inflammatory response; Haemophilia; Werner syndrome;
KW   asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome;
KW   renal disease; Preeclampsia; cardiac allograft vascular disease;
KW   colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
KW   immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
KW   nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200177375-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-EP03968.
XX
PR   06-APR-2000; 2000DE-1019058.
PR   07-APR-2000; 2000DE-1019173.
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-017470/02.
XX
PT   New nucleic acid sequences from chemically modified genes associated
PT   with gene regulation, useful for analysing cytosine methylations for
PT   diagnosis and therapy of diseases e.g. severe combined immunodeficiency
PT   disease  -
XX
PS   Claim 1; SEQ ID No 67; 26pp; English.
XX
CC   The invention relates to 224 nucleic acid sequences comprising at least
CC   18 bases of a chemically pretreated gene associated with gene regulation
CC   selected from 43 known genes (or complementary sequences). The
CC   chemical pretreatment converts cytosine bases unmethylated at the
CC   5-position to uracil or another base with hybridisation behaviour
CC   dissimilar to cytosine, to enable analysis of cytosine methylations.
```

CC The DNA sequences, oligomers (or sets/arrays) and method are
CC useful in the diagnosis of diseases (or predisposition to diseases)
CC associated with gene regulation and in therapy of such diseases, by
CC enabling analysis of the cytosine methylation patterns of such genes,
CC kits are provided. They are especially useful in diagnosis
CC and therapy of e.g. severe combined immunodeficiency disease, cardiac
CC disorders, haemophilia, solid tumours and cancer, Werner syndrome,
CC asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease,
CC preeclampsia, graft versus-host disease. The present sequence is a
CC sequence included in the sequence data for this specification and is
CC associated with the human gene regulation-associated genes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 6350 BP; 1413 A; 356 C; 1779 G; 2802 T; 0 other;

Query Match 12.1%; Score 37.8; DB 24; Length 6350;
Best Local Similarity 46.4%; Pred. No. 6.1;
Matches 123; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

```
Qy     47 tttagatatagaaatatctgatgctgtcttcttcactaaattttgattacatgatttgac 106
          |||   | ||||||  | | | | | | || ||   |||| ||| |||      |   |
Db    681 ttttattgtagaaagttttaaagatttttttttttttaaaatttaatttttatttgaaat 740

Qy    107 agcaatattgaagagtctaacagccagcacgcaggttggtaagtactgtgggaacatcac 166
          |    |||| ||| || |   ||   | |       |  |       |     | ||
Db    741 aattgtatttaagggtttttagtaggtaaagtatatatttttataaggttttaaatttt 800

Qy    167 agattttggctccatgccctaaagagaaattggctttcagattatttggattaaaaacaa 226
          |||||||   |        ||||  ||   |  |||     | | || ||| | |
Db    801 agatttttaataatgtatttaaattgagtatttttttttttgtgtatgtatttattattt 860

Qy    227 agactttcttaagagatgtaaaattttcatgatgttttctttttgctaaaactaaagaa 286
          | |||  | |   || | |||||||  |  | ||   |||||||  | |  | |   |
Db    861 gtagttttattatttatattaaattttagtttttttagttttttgaaatacgttagtga 920

Qy    287 ttaacgcgtattcttttacatttca 311
          |     ||| |  || |   || |
Db    921 atttttagtagttattaattattta 945
```

RESULT 13
AAH33046
ID AAH33046 standard; cDNA; 544 BP.
XX
AC AAH33046;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:102.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG73615.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 2284; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 544 BP; 180 A; 68 C; 102 G; 189 T; 5 other;

Query Match 12.1%; Score 37.6; DB 22; Length 544;
Best Local Similarity 51.8%; Pred. No. 4.3;
Matches 85; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

```
Qy    148 agtactgtgggaacatcacagattttggctccatgccctaaagagaaattggctttcaga 207
          || |||   ||| |  |   | |   ||      || | | ||| |||||   | |
Db     67 agaactagtggatccccccgggctgcaggaattcggcacgagagaaaaattatttgtatat 126

Qy    208 ttatttggattaaaaacaaagactttcttaagagatgtaaaattttcatgatgttttctt 267
             |||  |   |  | || | |||| |  |||| | | |  |||  |  ||  ||| ||
Db    127 aactttaaaaggagtagaagggctttttgcagagttattacgtttgaagtatactttatt 186

Qy    268 ttttgctaaaactaaagaattaacgcgtattcttttacatttca 311
          | |||  |||| || ||| ||   |   ||  |  |  | ||||
Db    187 tcttgaaaaaattacagatttttgtaaataatgatgtaattca 230
```

RESULT 14
AAI58419
ID AAI58419 standard; cDNA; 6799 BP.
XX
AC AAI58419;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 622.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM39263.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 622; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 6799 BP; 1825 A; 1455 C; 1710 G; 1809 T; 0 other;

Query Match 12.0%; Score 37.4; DB 22; Length 6799;
Best Local Similarity 67.1%; Pred. No. 7.7;
Matches 53; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 188 aagagaaattggctttcagattatttggattaaaaacaaagactttcttaagagatgtaa 247
Db 5217 atgagtagttgtgttacagttcatttttctttaaaaaaaagtactttgagaaaaggtgcaa 5276

Qy 248 aattttcatgatgttttct 266
Db 5277 aatattcttgaaagtctct 5295

RESULT 15
AAI61373
ID AAI61373 standard; DNA; 513445 BP.
XX
AC AAI61373;
XX
DT 16-OCT-2001 (first entry)
XX
DE Soybean 318013 region A3, SEQ ID NO: 4.
XX
KW Soybean; antihelmintic; gene therapy; soybean cyst nematode; SCN;
KW SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;
KW 240017 region G3; 318013 region A3; 515002 region G2; ds.
XX
OS Glycine max.
XX
PN WO200151627-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US00552.
XX
PR 07-JAN-2000; 2000US-0174880.
XX
PA (MONS) MONSANTO CO.
XX
PI Hauge BM, Wang ML, Parsons JD, Parnell LD;
XX
DR WPI; 2001-425872/45.
DR P-PSDB; AAM42216.
XX
PT New purified nucleic acid for producing a soybean plant having soybean
PT cyst nematode resistance and for use in plant breeding programs -
XX
PS Claim 30; Page 596-893; 1353pp; English.
XX
CC The invention relates to nucleic acid molecules from regions of the
CC soybean genome which are associated with soybean cyst nematode (SCN)
CC resistance. The nucleic acids are used to transform plants, and can
CC produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.
CC The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes
CC of soybean plants and for introgressing SCN resistance or partial SCN
CC resistance into soybean plants. They can also be used in plant breeding
CC programmes. The invention also relates to proteins encoded by such
CC nucleic acid molecules, as well as antibodies capable of recognising
CC these proteins. The present sequence is a nucleic acid molecule
CC provided in the specification.
XX
SQ Sequence 513445 BP; 173367 A; 85402 C; 83912 G; 170492 T; 272 other;

Query Match 12.0%; Score 37.4; DB 22; Length 513445;
Best Local Similarity 53.0%; Pred. No. 17;
Matches 80; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 159 aacatcacagattttggctccatgccctaaagagaaattggctttcagattatttggatt 218
Db 49203 atcattatatattactgatgtatcttttaggcactaatttgattatttactctttcaaaa 49262

Qy 219 aaaaacaaagactttcttaagagatgtaaaattttcatgatgttttctttttgctaaaa 278
Db 49263 taaataaaaatgtttcaaaataaaagcaatattaggttacttgtttatttcaacagaaaa 49322

Qy 279 ctaaagaattaacgcgtattcttttacattt 309
Db 49323 caaactgagtaacaaattgacttttacttttt 49353

Search completed: September 9, 2002, 20:15:04
Job time: 13982 sec